In The Specification:

Please amend the paragraph found on lines 19-23 of page 12 as follows

"*Lemna gibba*-preferred codons" as used herein refers to codons that have a frequency of codon usage in *Lemna gibba* of greater than 17% where the frequency of codon usage in *Lemna gibba* was obtained from the Codon Usage Database (GenBank Release 113,0; <u>see Table 5</u> at http://www.kazusa.or.jp/codon/cgibin/showcodon.cgi?species= Lemna+gibba+[gbpln]).

Please amend the paragraph on line 28 of page 17 through line 25 of page 18 as follows:

B.   Modification of Nucleotide Sequences for Enhanced Expression in Duckweed

The present invention provides for the modification of the expressed nucleotide sequence to enhance its expression in duckweed. One such modification is the synthesis of the nucleotide sequence of interest using duckweed-preferred codons. Methods are available in the art for synthesizing nucleotide sequences with plant-preferred codons. See, e.g., U.S. Patent Nos. 5,380,831 and 5,436,391; Perlak *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 15:3324; Iannacome *et al.* (1997) *Plant Mol. Biol.* 34:485; and Murray *et al.*, (1989) *Nucleic Acids. Res.* 17:477, herein incorporated by reference. The preferred codons may be determined from the codons of highest frequency in the proteins expressed in duckweed. For example, the frequency of codon usage for *Lemna gibba* <u>for GenBank Release 113.0</u> is found <u>in Table 5.</u> on the web page: http://www.kazusa.or.jp/codon/cgi-bin/showcodon.cgi?species= Lemna+gibba+[gbpln], and the frequency of codon usage for *Lemna minor* is found on the web page http://www.kazusa.or.jp/codon/cgibin/showcodon.cgi?species= Lemna+minor+[gbpln]. It is recognized that genes which have been optimized for expression in duckweed and other monocots can be used in the methods of the invention. See, e.g., EP 0 359 472, EP 0 385 962, WO 91/16432; Perlak *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88:3324; Iannacome *et al.* (1997) *Plant Mol. Biol.* 34:485; and Murray *et al.* (1989) *Nuc. Acids Res.* 17:477, and the like, herein incorporated by reference. It is further recognized that all or any part of the gene sequence may be optimized or synthetic. In other words, fully optimized or partially

optimized sequences may also be used. For example, 40 %, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 87%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% of the codons may be duckweed-preferred codons. In one embodiment, between 90 and 96 % of the codons are duckweed-preferred codons. The coding sequence of the nucleotide sequence of interest may comprise codons used with a frequency of at least 17% in *Lemna gibba*. In one embodiment, the modified nucleotide sequence is the human α-2B-interferon encoding nucleotide sequence shown in SEQ ID NO:2, which contains 93% duckweed preferred codons.

Please amend the paragraph on lines 23-27 of page 25 as follows

The expression vector pBMSP-3, also used in some of the following examples, contains the components of the pBMSP-1 expression vector described above and additionally contains a nucleotide sequence corresponding to nucleotides 1222-1775 of the maize alcohol dehydrogenase gene (GenBank Accession Number X04049) inserted between the promoter and the polylinker. This sequence is shown in SEQ ID NO:9.

Please amend Table 1 on page 27 as follows:

Table 1

Construct Name	Expression Vector	Signal Peptide	Interferon-encoding Sequence
IFN01	pBMSP-1	None	Non-optimized interferon (SEQ ID NO:10; nucleotides 580-1077 of GenBank Accession No. J00207)
IFN02	pBMSP-3	Non-optimized interferon (SEQ ID NO:11; nucleotides 511-579 of GenBank Accession No. J00207)	Non-optimized interferon (SEQ ID NO:10; nucleotides 580-1077 of GenBank Accession No. J00207)
IFN03	pBMSP-3	*Arabidopsis thaliana* endochitinase (SEQ ID NO:12; nucleotides 338-399 of GenBank Accession number AB023460 with an additional "A" added to the 3' end of the sequence)	Non-optimized interferon (SEQ ID NO:10; nucleotides 580-1077 of GenBank Accession No. J00207)
IFN05	pBMSP-3	Modified rice α-amylase * (encoding the amino acid sequence shown in SEQ ID NO:7)	Non-optimized interferon (SEQ ID NO:10; nucleotides 580-1077 of GenBank Accession No. J00207)
IFN07	pBMSP-3	Wild type rice α-amylase (nucleotides 34-126 of GenBank Accession No. M24286, encoding the amino acid sequence shown in SEQ ID NO:6)	Non-optimized interferon (SEQ ID NO:10; nucleotides 580-1077 of GenBank Accession No. J00207)
IFN08	pBMSP-3	Optimized wild type rice α-amylase (SEQ ID NO:3)	Non-optimized interferon (SEQ ID NO:10; nucleotides 580-1077 of GenBank Accession No. J00207)
IFN09	pBMSP-3	Optimized wild type rice α-amylase (SEQ ID NO:3)	Optimized interferon (SEQ ID NO:2)
IFN10	pBMSP-3	None	Optimized interferon (SEQ ID NO:2)
IFN11	pBMSP-1	Optimized wild type rice α-amylase (SEQ ID NO:3)	Optimized interferon (SEQ ID NO:2)
IFN12	pBMSP-1	None	Optimized interferon (SEQ ID NO:2)

Please insert the following table beginning on line 8 of page 34.

Table 5: *Lemna gibba*-**preferred codons from GenBank Release 113**

UUU 2.2	(	4)	UCU 0.5	(	1)	UAU 2.2	(	4)	UGU 0.0	(	0)
UUC 50.5	(	92)	UCC 31.9	(	58)	UAC 40.1	(	73)	UGC 17.6	(	32)
UUA 0.0	(	0)	UCA 0.5	(	1)	UAA 3.8	(	7)	UGA 1.6	(	3)
UUG 2.7	(	5)	UCG 15.4	(	28)	UAG 0.0	(	0)	UGG 24.2	(	44)
CUU 0.5	(	1)	CCU 6.6	(	12)	CAU 0.5	(	1)	CGU 1.1	(	2)
CUC 39.0	(	71)	CCC 43.4	(	79)	CAC 6.6	(	12)	CGC 26.9	(	49)
CUA 1.1	(	2)	CCA 2.2	(	4)	CAA 4.4	(	8)	CGA 1.1	(	2)
CUG 22.5	(	41)	CCG 20.9	(	38)	CAG 26.9	(	49)	CGG 7.7	(	14)
AUU 0.0	(	0)	ACU 3.3	(	6)	AAU 1.1	(	2)	AGU 0.0	(	0)
AUC 33.5	(	61)	ACC 26.4	(	48)	AAC 37.9	(	69)	AGC 22.0	(	40)
AUA 0.0	(	0)	ACA 0.5	(	1)	AAA 0.0	(	0)	AGA 4.9	(	9)
AUG 33.5	(	61)	ACG 9.3	(	17)	AAG 57.1	(	104)	AGG 6.0	(	11)
GUU 9.3	(	17)	GCU 7.1	(	13)	GAU 1.6	(	3)	GGU 1.1	(	2)
GUC 28.0	(	51)	GCC 73.6	(	134)	GAC 38.4	(	70)	GGC 46.7	(	85)
GUA 0.0	(	0)	GCA 5.5	(	10)	GAA 2.2	(	4)	GGA 1.1	(	2)
GUG 34.0	(	62)	GCG 20.9	(	38)	GAG 62.6	(	114)	GGG 27.5	(	50)